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Entry history

[Entry info] [Name and origin] [References] [Comments] [Cross-references] [Keywords] [Features] [Sequence] [Tools]

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Entry information

Entry name	FACE1_MOUSE
Primary accession number	Q80W54
Secondary accession numbers	Q8BJK4 Q8K569
Integrated into Swiss-Prot on	September 13, 2005
Sequence was last modified on	September 13, 2005 (Sequence version 2)
Annotations were last modified on	September 2, 2008 (Entry version 35)

Name and origin of the protein

Protein name	CAAX prenyl protease 1 homolog
Synonyms	EC 3.4.24.84
	Prenyl protein-specific endoprotease 1
	Farnesylated proteins-converting enzyme 1
	FACE-1
	Zinc metalloproteinase Ste24 homolog
Gene name	Name: Zmpste24
	Synonyms: Face1
From	Mus musculus (Mouse) [TaxID: 10090]
Taxonomy	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi Muroidea; Muridae; Murinae; Mus.
Protein existence	1: Evidence at protein level;

References

[1] NUCLEOTIDE SEQUENCE [MRNA].
   DOI=10.1074/jbc.M102908200; PubMed=11399759 [NCBI, ExPASy, EBI, Israel, Japan]
   Leung G.K., Schmidt W.K., Bergo M.O., Gavino B., Wong D.H., Tam A., Ashby M.N., Michaelis S., Young S.G.;
   "Biochemical studies of Zmpste24-deficient mice.";
   J. Biol. Chem. 276:29051-29058(2001).

[2] NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION IN LAMIN A/C PROCESSING.

STRAIN=C57BL/6;
DOI=10.1038/ng871; PubMed=11923874 [NCBI, ExPASy, EBI, Israel, Japan]
Pendas A.M., Zhou Z., Cadinanos J., Freije J.M.P., Wang J., Hultenby K., Astudillo A., Wernerson A., Rodriguez F., Triggvason K., Lopez-Otin C.;
"Defective prelamin A processing and muscular and adipocyte alterations in Zmpste24 metalloproteinas deficient mice.";
Nat. Genet. 31:94-99(2002).
[3] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
STRAIN=C57BL/6J;
DOI=10.1126/science.1112014; PubMed=16141072 [NCBI, ExPASy, EBI, Israel, Japan]
Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhar B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., ▨, Hayashizaki Y.;
"The transcriptional landscape of the mammalian genome.";
Science 309:1559-1563(2005).

Comments

- *FUNCTION*: Proteolytically removes the C-terminal three residues of farnesylated proteins. Acts on lamin A/C.
- *CATALYTIC ACTIVITY*: The peptide bond hydrolyzed can be designated -C-|-A-A-X in which C is an S-isoprenylated cysteine residue, A is usually aliphatic and X is the C-terminal residue of the substra protein, and may be any of several amino acids.
- *COFACTOR*: Binds 1 zinc ion per subunit *(By similarity)*.
- *SUBCELLULAR LOCATION*: Endoplasmic reticulum membrane; Multi-pass membrane protein *(By similarity)*. Golgi apparatus membrane; Multi-pass membrane protein *(By similarity)*.
- *SIMILARITY*: Belongs to the peptidase M48A family [view classification].

Copyright

Cross-references

Sequence databases

EMBL	AY029194; AAK38172.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]
	AJ487544; CAD31792.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]
	AK083566; BAC38953.1; -; mRNA.[EMBL / GenBank / DDBJ] [CoDingSequence]
RefSeq	NP_766288.1; -.
UniGene	Mm.34399

3D structure databases

| ModBase | Q80W54. |

Protein family/group databases

| MEROPS | M48.003; -. |

Organism-specific databases

| MGI | MGI:1890508; Zmpste24. |

Gene expression databases

| ArrayExpress | Q80W54; -. |
| GermOnline | ENSMUSG00000043207; Mus musculus. |

Ontologies

GO	GO:0005624; Cellular component: membrane fraction *(inferred from direct assay from MGI)*
	GO:0004222; Molecular function: metalloendopeptidase activity *(inferred from direct assay from MGI)*.
	GO:0006998; Biological process: nuclear membrane organization *(inferred from genetic interaction from MGI)*.

GO:0030327; Biological process: prenylated protein catabolic process *(inferred from direct assay from MGI)*.

QuickGo view.

Family and domain databases

InterPro	IPR006025; Pept_M_Zn_BS. IPR001915; Peptidase_M48. Graphical view of domain structure.
Pfam	PF01435; Peptidase_M48; 1. Pfam graphical view of domain structure.
PROSITE	PS00142; ZINC_PROTEASE; FALSE_NEG.
BLOCKS	Q80W54.

Genome annotation databases

Ensembl	ENSMUSG00000043207; Mus musculus. [Contig view]
GeneID	230709; -.
KEGG	mmu:230709; -.

Phylogenomic databases

HOGENOM	Q80W54; -.
HOVERGEN	Q80W54; -.

Other

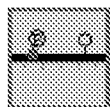|	
SOURCE	Zmpste24; Mus musculus.
ProtoNet	Q80W54.
UniRef	View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Endoplasmic reticulum; Golgi apparatus; Hydrolase; Membrane; Metal-binding; Metalloprotease; Protease; Transmembrane; Zinc.

Features

Feature table viewer   Feature aligner

Key	From	To	Length	Description	FTId
CHAIN	1	475	475	CAAX prenyl protease 1 homolog.	PRO_0000138845
TRANSMEM	19	39	21	*Potential.*	
TRANSMEM	82	102	21	*Potential.*	
TRANSMEM	124	144	21	*Potential.*	
TRANSMEM	171	191	21	*Potential.*	
TRANSMEM	196	216	21	*Potential.*	
TRANSMEM	348	368	21	*Potential.*	
TRANSMEM	383	405	23	*Potential.*	
ACT_SITE	336	336		*By similarity.*	
ACT_SITE	419	419		Proton donor *(By similarity)*.	
METAL	335	335		Zinc; catalytic *(By similarity)*.	
METAL	339	339		Zinc; catalytic *(By similarity)*.	
METAL	415	415		Zinc; catalytic *(By similarity)*.	
CONFLICT	53	53		A -> S (in Ref. 2; CAD31792).	
CONFLICT	153	153		H -> Q (in Ref. 1; AAK38172).	
CONFLICT	157	157		H -> Q (in Ref. 1; AAK38172).	

Sequence information

Length: 475 AA [This is the length of the unprocessed precursor]

Molecular weight: 54735 Da [This is the MW of the unprocessed precursor]

CRC64: 509B82D757FC7A4B [This i a checksum on the sequence]

```
         10         20         30         40         50         60
MGMWASVDAM WDFPAEKRIF GAVLLFSWTV YLWETFLAQR QRRIYKTTTR VPAELEQIMD

         70         80         90        100        110        120
SDTFEKSRLY QLDKSTFSFW SGLYSEVEGT FILLFGGIPY LWRLSGQFCS SAGFGPEYEI

        130        140        150        160        170        180
IQSLVFLLLA TLFSALTGLP WSLYNTFVIE EKHGFNHQTL EFFMKDAIKK FIVTQCILLP

        190        200        210        220        230        240
VSALLLYIIK IGGDYFFIYA WLFTLVVSLV LVTIYADYIA PLFDKFTPLP EGKLKQEIEV

        250        260        270        280        290        300
MAKSIDFPLT KVYVVEGSKR SSHSNAYFYG FFKNKRIVLF DTLLEEYSVP NKDNQEESGM

        310        320        330        340        350        360
EARNEGEGDS EEVKAKVKNK KQGCKNEEVL AVLGHELGHW KLGHTVKNII ISQMNSFLCF

        370        380        390        400        410        420
FLFAVLIGRR ELFAAFGFYD SQPTLIGLLI IFQFIFSPYN EVLSFCLTVL SRRFEFQADA

        430        440        450        460        470
FAKKLGKAKD LYSALIKLNK DNLGFPVSDW LFSTWHYSHP PLLERLQALK NAKQD
```

Q80W54 in FASTA format

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BLAST BLAST submission on ExPASy/SIB or at NCBI (USA)

Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)

ScanProsite, MotifScan

Submit a homology modeling request to SWISS-MODEL

NPSA Sequence analysis tools

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